

SEQUENCE LISTING



#4

<110> Glucksmann, Maria A.
Hodge, Martin G.

<120> 2871 RECEPTOR, A NOVEL G-PROTEIN COUPLED RECEPTOR

<130> 5800-2A (035800/183295)

<140> US 09/324,465

<141> 1999-06-02

<150> 09/088,857

<151> 1998-06-02

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 358

<212> PRT

<213> Homo sapiens

<400> 1

Met Gly Phe Asn Leu Thr Leu Ala Lys Leu Pro Asn Asn Glu Leu His

1 5 10 15

Gly Gln Glu Ser His Asn Ser Gly Asn Arg Ser Asp Gly Pro Gly Lys

20 25 30

Asn Thr Thr Leu His Asn Glu Phe Asp Thr Ile Val Leu Pro Val Leu

35 40 45

Tyr Leu Ile Ile Phe Val Ala Ser Ile Leu Leu Asn Gly Leu Ala Val

50 55 60

Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu

65 70 75 80

Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe

85 90 95

Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe Lys Phe Ile

100 105 110

Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser

115 120 125

Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu Lys Val Val
 130 135 140

Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val
 145 150 155 160

Leu Ser Val Cys Val Trp Val Ile Met Ala Val Leu Ser Leu Pro Asn
 165 170 175

Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu Asp Asn Ile His Asp Cys
 180 185 190

Ser Lys Leu Lys Ser Pro Leu Gly Val Lys Trp His Thr Ala Val Thr
 195 200 205

Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly
 210 215 220

Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe
 225 230 235 240

Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val
 245 250 255

Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg
 260 265 270

Ile Pro Phe Thr Phe Ser His Leu Asp Arg Leu Leu Asp Glu Ser Ala
 275 280 285

Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile Thr Leu Phe Leu Ser Ala
 290 295 300

Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met Cys Arg Ser
 305 310 315 320

Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu
 325 330 335

Ser Ile Arg Ser Leu Gln Ser Val Arg Arg Ser Glu Val Arg Ile Tyr
 340 345 350

Tyr Asp Tyr Thr Asp Val
 355

<210> 2

<211> 1489
 <212> DNA
 <213> Homo sapiens

<400> 2
 ccacgcgtcc ggagaatttg aaaggggtgcc ccaaaggaca atctctaaag gggtaagggg 60
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 ttccctgccg accttagttt caaagcttat tcttaattag agacaagaaa cctgtttcaa 180
 cttgaagaca ccgtatgagg tgaatggaca gccagccacc acaatgaaag aaatcaaacc 240
 aggaataacc tatgctgaac ccacgcctca atcgtcccca agtgtttcct gacacgcac 300
 tttgcttaca gtgcatcaca actgaagaat ggggttcaac ttgacgcttg caaaattacc 360
 aaataacgag ctgcacggcc aagagagtca caattcaggc aacaggagcg acgggccagg 420
 aaagaacacc acccttcaca atgaatttga cacaattgtc ttgccggtgc tttatctcat 480
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 gaataaaacc agcttcatat tctatctcaa aaacatagtg gttgcagacc tcataatgac 600
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 ccagagcatc aggggtgttg tggctgtgtt ttttacctgc tttctaccat atcacttgtg 1140
 cagaattcct tttactttta gtcacttaga caggctttta gatgaatctg cacaaaaaat 1200
 cctatattac tgcaaagaaa ttacactttt cttgtctgcg tgtaatgttt gcctggatcc 1260
 aataatttac tttttcatgt gtaggtcatt ttcaagaagg ctgttcaaaa aatcaaatat 1320
 cagaaccagg agtgaaagca tcagatcact gcaaagtgtg agaagatcgg aagttcgcac 1380
 atattatgat tacactgatg tgtaggcctt ttattgtttg ttggaatcga tatgtacaaa 1440
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<210> 3
 <211> 269
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: consensus
 sequence of the seven transmembrane domain
 rhodopsin superfamily from the Prosite data base

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 Gly Asn Ile Leu Val Ile Trp Val Ile Cys Arg Tyr Arg Arg Met Arg
 1 5 10 15
 Thr Pro Met Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu
 20 25 30

Phe Ser Leu Phe Thr Met Pro Phe Trp Met Val Tyr Tyr Val Met Gln
35 40 45

Gly Arg Trp Pro Phe Gly Asp Phe Met Cys Arg Ile Trp Met Tyr Phe
50 55 60

Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr Cys Ile Ser
65 70 75 80

Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg Tyr Met Arg
85 90 95

Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile Ile Ile Trp
100 105 110

Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met Phe Arg Trp
115 120 125

Ser Thr Tyr Arg Asp Glu Asn Glu Trp Asn Met Thr Trp Cys Met Ile
130 135 140

Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile Leu Met Thr
145 150 155 160

Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu Phe Cys Tyr
165 170 175

Trp Arg Ile Tyr Arg Ile Ala Arg Leu Trp Met Arg Met Ile Pro Ser
180 185 190

Trp Gln Arg Arg Arg Arg Met Ser Met Arg Arg Glu Arg Arg Ile Val
195 200 205

Lys Met Leu Ile Ile Ile Met Val Val Phe Ile Ile Cys Trp Leu Pro
210 215 220

Tyr Phe Ile Val Met Phe Met Asp Thr Leu Met Met Trp Trp Phe Cys
225 230 235 240

Glu Phe Cys Ile Trp Arg Arg Leu Trp Met Tyr Ile Phe Glu Trp Leu
245 250 255

Ala Tyr Val Asn Cys Pro Cys Ile Asn Pro Ile Ile Tyr
260 265

<210> 4

<211> 20

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
oligonucleotide primer

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<210> 5

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
oligonucleotide primer

<400> 5

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<210> 6

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
oligonucleotide probe

<400> 6

agcattgatc gctatctgaa ggtggtcaa

29